



Pu/09

RAW SEQUENCE LISTING

DATE: 08/26/2002

PATENT APPLICATION: US/09/890,549

TIME: 14:01:22

Input Set : A:\pf0676usn_seqlist.txt

Output Set: N:\CRF3\08262002\I890549.raw

4 <110> APPLICANT: INCYTE PHARMACEUTICALS, INC.
 5 TANG, Y. Tom
 6 HILLMAN, Jennifer L.
 7 YUE, Henry
 8 AZIMZAI, Yalda
 9 BAUGHN, Mariah R.
 10 TRAN, Bao

12 <120> TITLE OF INVENTION: HUMAN LIPID-ASSOCIATED PROTEINS

14 <130> FILE REFERENCE: PF-0676 PCT

C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/890,549

C--> 17 <141> CURRENT FILING DATE: 2002-08-26

19 <150> PRIOR APPLICATION NUMBER: 60/120,703, 60/142,762

W--> 20 <151> PRIOR FILING DATE: 1999-02-19, 1999-07-08

22 <160> NUMBER OF SEQ ID NOS: 24

24 <170> SOFTWARE: PERL Program

26 <210> SEQ ID NO: 1

27 <211> LENGTH: 331

28 <212> TYPE: PRT

29 <213> ORGANISM: Homo sapiens

31 <220> FEATURE:

32 <221> NAME/KEY: misc_feature

33 <223> OTHER INFORMATION: Incyte ID No: 161190CD1

35 <400> SEQUENCE: 1

36 Met Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr

37 1 5 10 15

38 Phe Arg Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr

39 20 25 30

40 Asn Asn Glu Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro

41 35 40 45

42 Arg Asp Glu Ala Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg

43 50 55 60

44 Thr Tyr Ala Ala Ile Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu

45 65 70 75

46 Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Val Lys Arg

47 80 85 90

48 Lys Ile Gln Glu Ser Ile Glu Lys Leu Arg Ala Leu Ala Asn Gly

49 95 100 105

50 Ile Glu Glu Val His Arg Gly Cys Thr Ile Ser Asn Val Val Ser

51 110 115 120

52 Ser Ser Thr Gly Ala Ala Ser Gly Ile Met Ser Leu Ala Gly Leu

53 125 130 135

54 Val Leu Ala Pro Phe Thr Ala Gly Thr Ser Leu Ala Leu Thr Ala

55 140 145 150

Aug 17
2480
Does Not Comply
Corrected Diskette Needed

group these together

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56 Ala Gly Val Gly Leu Gly Ala Ala Ser Ala Val Thr Gly Ile Thr
57                               155                      160                      165
58 Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser Ala Glu Ala Glu
59                               170                      175                      180
60 Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu Lys Val Phe
61                               185                      190                      195
62 Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser Leu Leu
63                               200                      205                      210
64 Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile Arg
65                               215                      220                      225
66 Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr
67                               230                      235                      240
68 Trp Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile
69                               245                      250                      255
70 Ala Gly Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser
71                               260                      265                      270
72 Ala Thr Thr Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu
73                               275                      280                      285
74 Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Ala Ser
75                               290                      295                      300
76 Ala Glu Glu Leu Arg Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu
77                               305                      310                      315
78 Met Glu Leu Thr Gln Ile Tyr Gln Arg Leu Asn Pro Cys His Thr
79                               320                      325                      330

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80 His

83 <210> SEQ ID NO: 2

84 <211> LENGTH: 480

85 <212> TYPE: PRT

86 <213> ORGANISM: Homo sapiens

88 <220> FEATURE:

89 <221> NAME/KEY: misc_feature

90 <223> OTHER INFORMATION: Incyte ID No: 1292575CD1

92 <400> SEQUENCE: 2

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93 Met Asn Gly Glu Glu Glu Phe Phe Asp Ala Val Thr Gly Phe Asp
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95 Ser Asp Asn Ser Ser Gly Glu Phe Ser Glu Ala Asn Gln Lys Val
96                               20                      25                      30
97 Thr Gly Met Ile Asp Leu Asp Thr Ser Lys Asn Asn Arg Ile Gly
98                               35                      40                      45
99 Lys Thr Gly Glu Arg Pro Ser Gln Glu Asn Gly Ile Gln Lys His
100                              50                      55                      60
101 Arg Thr Ser Leu Pro Ala Pro Met Phe Ser Arg Ser Asp Phe Ser
102                              65                      70                      75
103 Val Trp Thr Ile Leu Lys Lys Cys Val Gly Leu Glu Leu Ser Lys
104                              80                      85                      90
105 Ile Thr Met Pro Ile Ala Phe Asn Glu Pro Leu Ser Phe Leu Gln
106                              95                      100                     105
107 Arg Ile Thr Glu Tyr Met Glu His Val Tyr Leu Ile His Arg Ala
108                             110                      115                      120

```

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109	Ser	Cys	Gln	Pro	Gln	Pro	Leu	Glu	Arg	Met	Gln	Ser	Val	Ala	Ala
110					125					130					135
111	Phe	Ala	Val	Ser	Ala	Val	Ala	Ser	Gln	Trp	Glu	Arg	Thr	Gly	Lys
112					140					145					150
113	Pro	Phe	Asn	Pro	Leu	Leu	Gly	Glu	Thr	Tyr	Glu	Leu	Ile	Arg	Glu
114					155					160					165
115	Asp	Leu	Gly	Phe	Arg	Phe	Ile	Ser	Glu	Gln	Val	Ser	His	His	Pro
116					170					175					180
117	Pro	Ile	Ser	Ala	Phe	His	Ser	Glu	Gly	Leu	Asn	His	Asp	Phe	Leu
118					185					190					195
119	Phe	His	Gly	Ser	Ile	Tyr	Pro	Lys	Leu	Lys	Phe	Trp	Gly	Lys	Ser
120					200					205					210
121	Val	Glu	Ala	Glu	Pro	Arg	Gly	Thr	Ile	Thr	Leu	Glu	Leu	Leu	Lys
122					215					220					225
123	His	Asn	Glu	Ala	Tyr	Thr	Trp	Thr	Asn	Pro	Thr	Cys	Cys	Val	His
124					230					235					240
125	Asn	Val	Ile	Ile	Gly	Lys	Leu	Trp	Ile	Glu	Gln	Tyr	Gly	Thr	Val
126					245					250					255
127	Glu	Ile	Leu	Asn	His	Arg	Thr	Gly	His	Lys	Cys	Val	Leu	His	Phe
128					260					265					270
129	Lys	Pro	Cys	Gly	Leu	Phe	Gly	Lys	Glu	Leu	His	Lys	Val	Glu	Gly
130					275					280					285
131	His	Ile	Gln	Asp	Lys	Asn	Lys	Lys	Lys	Leu	Phe	Met	Ile	Tyr	Gly
132					290					295					300
133	Lys	Trp	Thr	Glu	Cys	Leu	Trp	Gly	Ile	Asp	Pro	Val	Ser	Tyr	Glu
134					305					310					315
135	Ser	Phe	Lys	Lys	Gln	Glu	Arg	Arg	Gly	Asp	His	Leu	Arg	Lys	Ala
136					320					325					330
137	Lys	Leu	Asp	Glu	Asp	Ser	Gly	Lys	Ala	Asp	Ser	Asp	Val	Ala	Asp
138					335					340					345
139	Asp	Val	Pro	Val	Ala	Gln	Glu	Thr	Val	Gln	Val	Ile	Pro	Gly	Ser
140					350					355					360
141	Lys	Leu	Leu	Trp	Arg	Ile	Asn	Thr	Arg	Pro	Pro	Asn	Ser	Ala	Gln
142					365					370					375
143	Met	Tyr	Asn	Phe	Thr	Ser	Phe	Thr	Val	Ser	Leu	Asn	Glu	Leu	Glu
144					380					385					390
145	Thr	Gly	Met	Glu	Lys	Thr	Leu	Pro	Pro	Thr	Asp	Cys	Arg	Leu	Arg
146					395					400					405
147	Pro	Asp	Ile	Arg	Gly	Met	Glu	Asn	Gly	Asn	Met	Asp	Leu	Ala	Ser
148					410					415					420
149	Gln	Glu	Lys	Glu	Arg	Leu	Glu	Glu	Lys	Gln	Arg	Glu	Ala	Arg	Arg
150					425					430					435
151	Glu	Arg	Ala	Lys	Glu	Glu	Ala	Glu	Trp	Gln	Thr	Arg	Trp	Phe	Tyr
152					440					445					450
153	Pro	Gly	Asn	Asn	Pro	Tyr	Thr	Gly	Thr	Pro	Asp	Trp	Leu	Tyr	Ala
154					455					460					465
155	Gly	Asp	Tyr	Phe	Glu	Arg	Asn	Phe	Ser	Asp	Cys	Pro	Asp	Ile	Tyr
156					470					475					480
159	<210> SEQ ID NO: 3														

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Input Set : A:\pf0676usn_seqlist.txt

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160 <211> LENGTH: 409

161 <212> TYPE: PRT

162 <213> ORGANISM: Homo sapiens

164 <220> FEATURE:

165 <221> NAME/KEY: misc_feature

166 <223> OTHER INFORMATION: Incyte ID No: 2454393CD1

168 <400> SEQUENCE: 3

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169 Met Ala Thr Ser Val Gly His Arg Cys Leu Gly Leu Leu His Gly
170   1           5           10           15
171 Val Ala Pro Trp Arg Ser Ser Leu His Pro Cys Glu Ile Thr Ala
172           20           25           30
173 Leu Ser Gln Ser Leu Gln Pro Leu Arg Lys Leu Pro Phe Arg Ala
174           35           40           45
175 Phe Arg Thr Asp Ala Arg Lys Ile His Thr Ala Pro Ala Arg Thr
176           50           55           60
177 Met Phe Leu Leu Arg Pro Leu Pro Ile Leu Leu Val Thr Gly Gly
178           65           70           75
179 Gly Tyr Ala Gly Tyr Arg Gln Tyr Glu Lys Tyr Arg Glu Arg Glu
180           80           85           90
181 Leu Glu Lys Leu Gly Leu Glu Ile Pro Pro Lys Leu Ala Gly His
182           95          100          105
183 Trp Glu Val Ala Leu Tyr Lys Ser Val Pro Thr Arg Leu Leu Ser
184          110          115          120
185 Arg Ala Trp Gly Arg Leu Asn Gln Val Glu Leu Pro His Trp Leu
186          125          130          135
187 Arg Arg Pro Val Tyr Ser Leu Tyr Ile Trp Thr Phe Gly Val Asn
188          140          145          150
189 Met Lys Glu Ala Ala Val Glu Asp Leu His His Tyr Arg Asn Leu
190          155          160          165
191 Ser Glu Phe Phe Arg Arg Lys Leu Lys Pro Gln Ala Arg Pro Val
192          170          175          180
193 Cys Gly Leu His Ser Val Ile Ser Pro Ser Asp Gly Arg Ile Leu
194          185          190          195
195 Asn Phe Gly Gln Val Lys Asn Cys Glu Val Glu Gln Val Lys Gly
196          200          205          210
197 Val Thr Tyr Ser Leu Glu Ser Phe Leu Gly Pro Arg Met Cys Thr
198          215          220          225
199 Glu Asp Leu Pro Phe Pro Pro Ala Ala Ser Cys Asp Ser Phe Lys
200          230          235          240
201 Asn Gln Leu Val Thr Arg Glu Gly Asn Glu Leu Tyr His Cys Val
202          245          250          255
203 Ile Tyr Leu Ala Pro Gly Asp Tyr His Cys Phe His Ser Pro Thr
204          260          265          270
205 Asp Trp Thr Val Ser His Arg Arg His Phe Pro Gly Ser Leu Met
206          275          280          285
207 Ser Val Asn Pro Gly Met Ala Arg Trp Ile Lys Glu Leu Phe Cys
208          290          295          300
209 His Asn Glu Arg Val Val Leu Thr Gly Asp Trp Lys His Gly Phe
210          305          310          315

```

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```

211 Phe Ser Leu Thr Ala Val Gly Ala Thr Asn Val Gly Ser Ile Arg
212                               320                325                330
213 Ile Tyr Phe Asp Arg Asp Leu His Thr Asn Ser Pro Arg His Ser
214                               335                340                345
215 Lys Gly Ser Tyr Asn Asp Phe Ser Phe Val Thr His Thr Asn Arg
216                               350                355                360
217 Glu Gly Val Pro Met Arg Lys Gly Glu His Leu Gly Glu Phe Asn
218                               365                370                375
219 Leu Gly Ser Thr Ile Val Leu Ile Phe Glu Ala Pro Lys Asp Phe
220                               380                385                390
221 Asn Phe Gln Leu Lys Thr Gly Gln Lys Ile Arg Phe Gly Glu Ala
222                               395                400                405
223 Leu Gly Ser Leu
226 <210> SEQ ID NO: 4
227 <211> LENGTH: 759
228 <212> TYPE: PRT
229 <213> ORGANISM: Homo sapiens
231 <220> FEATURE:
232 <221> NAME/KEY: misc_feature
233 <223> OTHER INFORMATION: Incyte ID No: 2766980CD1
235 <400> SEQUENCE: 4
236 Met Glu Ser Ser Pro Phe Asn Arg Arg Gln Trp Thr Ser Leu Ser
237   1      5      10
238 Leu Arg Val Thr Ala Lys Glu Leu Ser Leu Val Asn Lys Asn Lys
239      20      25      30
240 Ser Ser Ala Ile Val Glu Ile Phe Ser Lys Tyr Gln Lys Ala Ala
241      35      40      45
242 Glu Glu Thr Asn Met Glu Lys Lys Arg Ser Asn Thr Glu Asn Leu
243      50      55      60
244 Ser Gln His Phe Arg Lys Gly Thr Leu Thr Val Leu Lys Lys Lys
245      65      70      75
246 Trp Glu Asn Pro Gly Leu Gly Ala Glu Ser His Thr Asp Ser Leu
247      80      85      90
248 Arg Asn Ser Ser Thr Glu Ile Arg His Arg Ala Asp His Pro Pro
249      95     100     105
250 Ala Glu Val Thr Ser His Ala Ala Ser Gly Ala Lys Ala Asp Gln
251     110     115     120
252 Glu Glu Gln Ile His Pro Arg Ser Arg Leu Arg Ser Pro Pro Glu
253     125     130     135
254 Ala Leu Val Gln Gly Arg Tyr Pro His Ile Lys Asp Gly Glu Asp
255     140     145     150
256 Leu Lys Asp His Ser Thr Glu Ser Lys Lys Met Glu Asn Cys Leu
257     155     160     165
258 Gly Glu Ser Arg His Glu Val Glu Lys Ser Glu Ile Ser Glu Asn
259     170     175     180
260 Thr Asp Ala Ser Gly Lys Ile Glu Lys Tyr Asn Val Pro Leu Asn
261     185     190     195
262 Arg Leu Lys Met Met Phe Glu Lys Gly Glu Pro Thr Gln Thr Lys
263     200     205     210

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/26/2002
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Input Set : A:\pf0676usn_seqlist.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; N Pos. 1237

VERIFICATION SUMMARY

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L:16 M:270 C: Current Application Number differs, Replaced Current Application Number
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:20 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:1080 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:1081 M:283 W: Missing Blank Line separator, <220> field identifier
L:1111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:1200